



PCT

RAW SEQUENCE LISTING

DATE: 05/15/2003

PATENT APPLICATION: US/10/088,920A

TIME: 13:50:01

Input Set : A:\25835104.app

Output Set: N:\CRF4\05152003\J088920A.raw

3 #110# APPLICANT: KIMAKI, NORIYUKI

4 YASOHARA, YOSHIEKO

5 HASEGAWA, JUNZO

6 #120# TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

7 #130# FILE REFERENCE: 025215/0104

8 #140# CURRENT APPLICATION NUMBER: 10/088,920A

9 #141# CURRENT FILING DATE: 2002-06-03

10 #150# PRIOR APPLICATION NUMBER: PCT/JPC1/06619

11 #151# PRIOR FILING DATE: 2001-08-01

12 #160# PRIOR APPLICATION NUMBER: JP 2000-232756

13 #151# PRIOR FILING DATE: 2000-08-01

14 #160# NUMBER OF SEQ ID NOS: 11

15 #210# SEQ ID NO: 1

16 #211# LENGTH: 277

17 #212# TYPE: CDS

18 #213# ORGANISM: Micrococcus luteus

19 #400# SEQUENCE: 1

20 Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

21 1 5 10 15

22 Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

23 20 25 30

24 Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

25 35 40 45

26 Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

27 50 55 60

28 Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

29 65 70 75 80

30 Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

31 85 90 95

32 Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp

33 100 105 110

34 Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu

35 115 120 125

36 Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Ile Asp Ile

37 130 135 140

38 Arg Ala Leu Ile Thr Thr Asp Thr Ile Thr Thr Thr Thr Thr Thr

39 145 150 155 160

40 Thr Asp Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr

41 165 170 175

42 Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Leu

43 180 185 190

44 Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val

45 195 200 205

ENTERED

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```

67 Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val
68      110      215      220
70 Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
71 225      230      235      240
72 His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
73      245      250      255
74 Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
75      260      265      270
76 Pro Leu Glu Met Leu
80      275
81 110: SEQ ID NO: 2
82 110: LENGTH: 1410
83 110: TYPE: DNA
84 110: ORGANISM: Micrococcus luteus
85 110: FEATURE:
86 110: NAME/KEY: CDS
87 110: LOCATION: (108)..(933)
88 110: SEQUENCE: 2
89 ggtaacccgac gacatcttat aagccagcac cggctcagga cgcgcaggcc ctccagagat 60
90 ctccagccac gtccgcctc aggaacaaca gaaggaagtg atcgagg atg cga cgg 116
91      Met Arg Arg
92      1
93 arg ccc ctg cag agt ggg gag tcc atc cct gta ctg ggt cag ggc acc 164
94 Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly Gln Gly Thr
95      10      15
96 tgg gac tgg ggt gac gac ccc ggc cgc cgc ggc gac gag gcc gcc gag 212
97 Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu Val Ala Ala
98 20      25      30      35
99 ctg ccc gcc ggc ctc gag ctg ggc atg aag ctg gtc gac acc gcc gag 260
100 Leu His Ala Gly Glu Leu Gly Met Thr Leu Val Asp Thr Ala Glu
101      40      45      50
102 arg tcc gcc gac gcc ggt ggc gag gag gtc ggt ggt gaa gca ttg gcg 308
103 Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu Ala Leu Ala
104      55      60      65
105 ggt cgc cgc gac gag gcc ttc gtc gtc agc aag gtc atg cgc tcc ccc 356
106 Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met Pro Ser His
107      70      75      80
108 gcc tcc cgt tcc gcc aag atc gcc gcc tgc gaa cgc agc ctg aaa cgc 404
109 Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser Leu Lys Arg
110      85      90      95
111 ctg gcc acc cat cgc atc gac ctc tac ctg ctg ccc tgg ccc gcc agg 452
112 Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp Gln Gly Arg
113 100      105      110      115
114 tcc cgc ctg cag gat acc gtc gcc gcc ttc ccc cag ctc gcc gag gac 500
115 Tyr Pro Leu Gln Asn Thr Val Ala Ala Phe His Gln Leu Val Glu Asp
116      120      125      130
117 ggc aaa atc cca tac tgg gcc ctc agc aac ttc ccc ccc cgc gcc ctc 548
118 Arg Lys Val Ala Tyr His Gly Val Thr Ala Leu Tyr Val Val Val Val
119      135      140      145

```

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```

135 gcc aag ctg aag gac gtg ccg gcc acc agc ggg ctg acc acg gat cag 596
136 Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr Thr Asp Gln
137 150 155 160
138 gtc ctg tac aac ctg tgc cgg cga gga ccg gac tac gac ctg ctg ccg 644
139 Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp Leu Leu Pro
140 165 170 175
141 tgg tgc gcc aac cac cag ctg ccg gtc atg gcc tac tgc ccg atc gag 697
142 Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser Pro Ile Glu
143 180 185 190 195
144 cag agc cgc atc att gac gac aac acc ctg aac gac gtc ggc gcc cgt 741
145 Gln Cys Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val Ala Ala Arg
146 200 205 210
147 cag agc gtc agc ccc ggc gcc gcc gcc gcc att gcc tgg gtg ctg cgc cgc 788
148 His Ser Val Ser Pro Ala Ala Ala Ala Leu Ala Trp Val Leu Arg Arg
149 215 220 225
150 gac tgc ctg tgc tgc aac atc ccc aag gcc agc agc cgc cag cag gtg cgc 836
151 Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln His Val Arg
152 230 235 240
153 gac aac gcc aac gca ctg gac gtg gag ctg acc cgc gaa gac ctg gat 884
154 Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu Asp Leu Asp
155 245 250 255
156 gcc ctg gac gcc gcc ttt ccg ccc ccg agc gga ccg cga cca ctg gaa 932
157 Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg Pro Leu Glu
158 260 265 270 275
159 att ctg tgc aac gac aac ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 980
160 Met Leu
161 ggc ggc ggc tgc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1028
162 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1116
163 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1164
164 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1252
165 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1340
166 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1428
167 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 1410
168 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
169 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
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179 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
180 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
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199 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc
200 ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc

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```

W--> 206 gayacngcng aratgtaygc                                20
209 <210> SEQ ID NO: 4
210 <211> LENGTH: 26
211 <212> TYPE: DNA
212 <213> ORGANISM: Artificial Sequence
214 <220> FEATURE:
215 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
217 <220> FEATURE:
218 <221> NAME/KEY: modified_base
219 <222> LOCATION: (6)
220 <223> OTHER INFORMATION: a, t, c, g, other or unknown
221 <220> FEATURE:
222 <221> NAME/KEY: modified_base
223 <222> LOCATION: (4)
224 <223> OTHER INFORMATION: a, t, c, g, other or unknown
227 <400> SEQUENCE: 4

W--> 228 tcytcnacna gytgrtgraa                                20
231 <210> SEQ ID NO: 5
232 <211> LENGTH: 26
233 <212> TYPE: DNA
234 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
237 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
239 <400> SEQUENCE: 1
240 <400> SEQUENCE: 1
241 <400> SEQUENCE: 1
242 <400> SEQUENCE: 1
243 <400> SEQUENCE: 1
244 <211> LENGTH: 26
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
249 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
251 <400> SEQUENCE: 6
252 <400> SEQUENCE: 6
253 <400> SEQUENCE: 6
254 <400> SEQUENCE: 6
255 <400> SEQUENCE: 6
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 46
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
263 <400> SEQUENCE: 7
264 <400> SEQUENCE: 7
265 <400> SEQUENCE: 7
266 <400> SEQUENCE: 7
267 <400> SEQUENCE: 7
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 29
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
275 <400> SEQUENCE: 8
276 <400> SEQUENCE: 8

```

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```

279 <210> SEQ ID NO: 9
280 <212> LENGTH: 144
281 <213> TYPE: DNA
282 <215> ORGANISM: Artificial Sequence
283 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
286     double-stranded DNA
288 <400> SEQUENCE: 9
289 caattctaaq gagatttaca tatgcgtcgt atgactttac catctggtga atctattcca    60
290 attttagctc aaggtacttg gggttgggtt gaagatccag gtcgtcgtgg tgatgaagtt    120
291 gctggtttac atgctggtct cgag                                144
294 <210> SEQ ID NO: 10
295 <212> LENGTH: 33
296 <213> TYPE: DNA
297 <215> ORGANISM: Artificial Sequence
298 <220> FEATURE:
300 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
301 <400> SEQUENCE: 10
302 caggagcttt aaggagggtt acaatgtata aag                                33
306 <210> SEQ ID NO: 11
307 <212> LENGTH: 28
308 <213> TYPE: DNA
309 <215> ORGANISM: Artificial Sequence
310 <220> FEATURE:
312 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
314 <400> SEQUENCE: 11
315 caaggatctt tatcgcgttc ctgcttgg                                28

```

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 6,9

Seq#:4; N Pos. 6,9